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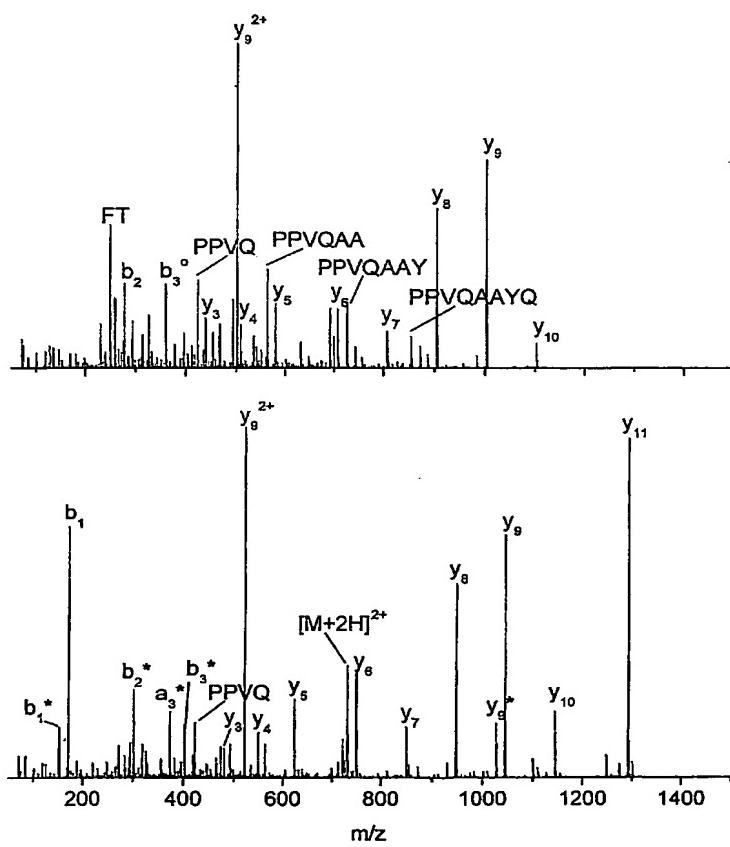
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(54) Title: PEPTIDE DERIVATIZATION FOR ENHANCING PROTEIN IDENTIFICATION BY MASS SPECTROMETRY



(57) Abstract: One aspect of the present invention is directed to a dual labeling strategy that enhances the mass spectrometry analysis of peptides, as demonstrated in Figure 2. In one embodiment a *de novosequencing* method is provided that utilizes both guanidination of lysine residues in conjunction with amidination of the N-termini of peptides to be analyzed by mass spectrometry. This approach facilitates identification of N- and C-terminal fragment ions.

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